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 aaaaaaatc tttgaaggga c 3121

<210> 7  
 <211> 830  
 <212> PRT  
 <213> Homo sapiens

<400> 7  
 Met Glu Gln Tyr Lys Leu Gln Ser Asp Arg Leu Arg Glu Gln Gln  
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 Glu Glu Met Val Glu Leu Arg Leu Arg Leu Glu Leu Val Arg Pro  
 20 25 30  
 Gly Trp Gly Gly Leu Arg Leu Leu Asn Gly Leu Pro Pro Gly Ser  
 35 40 45  
 Phe Val Pro Arg Pro His Thr Ala Pro Leu Gly Gly Ala His Ala  
 50 55 60  
 His Val Leu Gly Met Val Pro Pro Ala Cys Leu Pro Gly Asp Glu  
 65 70 75  
 Val Gly Ser Glu Gln Arg Gly Glu Gln Val Thr Asn Gly Arg Glu  
 80 85 90  
 Ala Gly Ala Glu Leu Leu Thr Glu Val Asn Arg Leu Gly Ser Gly  
 95 100 105

Ser Ser Ala Ala	Ser Glu Glu Glu Glu Glu Glu Glu Glu	Pro Pro
110	115	120
Arg Arg Thr Leu	His Leu Arg Arg Asn Arg Ile Ser Asn Cys Ser	
125	130	135
Gln Arg Ala Gly	Ala Arg Pro Gly Ser Leu Pro Glu Arg Lys Gly	
140	145	150
Pro Glu Leu Cys	Leu Glu Glu Leu Asp Ala Ala Ile Pro Gly Ser	
155	160	165
Arg Ala Val Gly	Gly Ser Lys Ala Arg Val Gln Ala Arg Gln Val	
170	175	180
Pro Pro Ala Thr	Ala Ser Glu Trp Arg Leu Ala Gln Ala Gln Gln	
185	190	195
Lys Ile Arg Glu	Leu Ala Ile Asn Ile Arg Met Lys Glu Glu Leu	
200	205	210
Ile Gly Glu Leu	Val Arg Thr Gly Lys Ala Ala Gln Ala Leu Asn	
215	220	225
Arg Gln His Ser	Gln Arg Ile Arg Glu Leu Glu Gln Glu Ala Glu	
230	235	240
Gln Val Arg Ala	Glu Leu Ser Glu Gly Gln Arg Gln Leu Arg Glu	
245	250	255
Leu Glu Gly Lys	Glu Leu Gln Asp Ala Gly Glu Arg Ser Arg Leu	
260	265	270
Gln Glu Phe Arg	Arg Arg Val Ala Ala Ala Gln Ser Gln Val Gln	
275	280	285
Val Leu Lys Glu	Lys Lys Gln Ala Thr Glu Arg Leu Val Ser Leu	
290	295	300
Ser Ala Gln Ser	Glu Lys Arg Leu Gln Glu Leu Glu Arg Asn Val	
305	310	315
Gln Leu Met Arg	Gln Gln Gln Gly Gln Leu Gln Arg Arg Leu Arg	
320	325	330
Glu Glu Thr Glu	Gln Lys Arg Arg Leu Glu Ala Glu Met Ser Lys	
335	340	345
Arg Gln His Arg	Val Lys Glu Leu Glu Leu Lys His Glu Gln Gln	
350	355	360
Gln Lys Ile Leu	Lys Ile Lys Thr Glu Glu Ile Ala Ala Phe Gln	
365	370	375
Arg Lys Arg Arg	Ser Gly Ser Asn Gly Ser Val Val Ser Leu Glu	
380	385	390
Gln Gln Gln Lys	Ile Glu Glu Gln Lys Lys Trp Leu Asp Gln Glu	



	395	400	405
Met Glu Lys Val	Leu Gln Gln Arg Arg	Ala Leu Glu Glu Leu Gly	
	410	415	420
Glu Glu Leu His	Lys Arg Glu Ala Ile	Leu Ala Lys Lys Glu Ala	
	425	430	435
Leu Met Gln Glu	Lys Thr Gly Leu Glu Ser	Lys Arg Leu Arg Ser	
	440	445	450
Ser Gln Ala Leu	Asn Glu Asp Ile Val	Arg Val Ser Ser Arg Leu	
	455	460	465
Glu His Leu Glu	Lys Glu Leu Ser Glu	Lys Ser Gly Gln Leu Arg	
	470	475	480
Gln Gly Ser Ala	Gln Ser Gln Gln Gln	Ile Arg Gly Glu Ile Asp	
	485	490	495
Ser Leu Arg Gln	Glu Lys Asp Ser Leu	Leu Lys Gln Arg Leu Glu	
	500	505	510
Ile Asp Gly Lys	Leu Arg Gln Gly Ser	Leu Leu Ser Pro Glu Glu	
	515	520	525
Glu Arg Thr Leu	Phe Gln Leu Asp Glu	Ala Ile Glu Ala Leu Asp	
	530	535	540
Ala Ala Ile Glu	Tyr Lys Asn Glu Ala	Ile Thr Cys Arg Gln Arg	
	545	550	555
Val Leu Arg Ala	Ser Ala Ser Leu Leu	Ser Gln Cys Glu Met Asn	
	560	565	570
Leu Met Ala Lys	Leu Ser Tyr Leu Ser	Ser Ser Glu Thr Arg Ala	
	575	580	585
Leu Leu Cys Lys	Tyr Phe Asp Lys Val	Val Thr Leu Arg Glu Glu	
	590	595	600
Gln His Gln Gln	Gln Ile Ala Phe Ser	Glu Leu Glu Met Gln Leu	
	605	610	615
Glu Glu Gln Gln	Arg Leu Val Tyr Trp	Leu Glu Val Ala Leu Glu	
	620	625	630
Arg Gln Arg Leu	Glu Met Asp Arg Gln	Leu Thr Leu Gln Gln Lys	
	635	640	645
Glu His Glu Gln	Asn Met Gln Leu Leu	Leu Gln Gln Ser Arg Asp	
	650	655	660
His Leu Gly Glu	Gly Leu Ala Asp Ser	Arg Arg Gln Tyr Glu Ala	
	665	670	675
Arg Ile Gln Ala	Leu Glu Lys Glu Leu	Gly Arg Tyr Met Trp Ile	
	680	685	690

Asn	Gln	Glu	Leu	Lys	Gln	Lys	Leu	Gly	Gly	Val	Asn	Ala	Val	Gly
				695					700					705
His	Ser	Arg	Gly	Gly	Glu	Lys	Arg	Ser	Leu	Cys	Ser	Glu	Gly	Arg
				710					715					720
Gln	Ala	Pro	Gly	Asn	Glu	Asp	Glu	Leu	His	Leu	Ala	Pro	Glu	Leu
				725					730					735
Leu	Trp	Leu	Ser	Pro	Leu	Thr	Glu	Gly	Ala	Pro	Arg	Thr	Arg	Glu
				740					745					750
Glu	Thr	Arg	Asp	Leu	Val	His	Ala	Pro	Leu	Pro	Leu	Thr	Trp	Lys
				755					760					765
Arg	Ser	Ser	Leu	Cys	Gly	Glu	Glu	Gln	Gly	Ser	Pro	Glu	Glu	Leu
				770					775					780
Arg	Gln	Arg	Glu	Ala	Ala	Glu	Pro	Leu	Val	Gly	Arg	Val	Leu	Pro
				785					790					795
Val	Gly	Glu	Ala	Gly	Leu	Pro	Trp	Asn	Phe	Gly	Pro	Leu	Ser	Lys
				800					805					810
Pro	Arg	Arg	Glu	Leu	Arg	Arg	Ala	Ser	Pro	Gly	Met	Ile	Asp	Val
				815					820					825
Arg	Lys	Asn	Pro	Leu										
				830										

<210> 8  
 <211> 662  
 <212> DNA  
 <213> Homo sapiens

<400> 8  
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 acagacgctc ctgttggttc aggactgtgg ctgtgccagc cgacacccag 150  
 gtgtgggaac aagatctaca acccttcaga gcagtgtgt tatgatgatg 200  
 ccatcttata cttaaaggag acccgccgct gtggctccac ctgcaccttc 250  
 tggcctgtct ttgagctctg ctgtcccag tcttttgcc ccagcagaa 300  
 gtttcttggtg aagttgaggg ttctgggtat gaagtctcag tgtcacttat 350  
 ctcccatctc ccggagctgt accaggaaca ggaggcacgt cctgtaccca 400  
 taaaaacccc aggctccact ggcagacggc agacaagggg agaagagacg 450  
 aagcagctgg acatcggaaga ctacagttga acttcggaga gaagcaactt 500  
 gacttcagag ggatgggtca atgacatagc tttggagagg agcccagctg 550

gggatggcca gacttcaggg gaagaatgcc ttctgcttc atcccccttc 600  
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 catttaccat ct 662

<210> 9  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 9  
 Met Arg Pro Arg Cys Cys Ile Leu Ala Leu Val Cys Trp Ile Thr  
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 Val Phe Leu Leu Gln Cys Ser Lys Gly Thr Thr Asp Ala Pro Val  
 20 25 30  
 Gly Ser Gly Leu Trp Leu Cys Gln Pro Thr Pro Arg Cys Gly Asn  
 35 40 45  
 Lys Ile Tyr Asn Pro Ser Glu Gln Cys Cys Tyr Asp Asp Ala Ile  
 50 55 60  
 Leu Ser Leu Lys Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe  
 65 70 75  
 Trp Pro Cys Phe Glu Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln  
 80 85 90  
 Gln Lys Phe Leu Val Lys Leu Arg Val Leu Gly Met Lys Ser Gln  
 95 100 105  
 Cys His Leu Ser Pro Ile Ser Arg Ser Cys Thr Arg Asn Arg Arg  
 110 115 120  
 His Val Leu Tyr Pro  
 125

<210> 10  
 <211> 1942  
 <212> DNA  
 <213> Homo sapiens

<400> 10  
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 ctgccgggtc tggagagctc cccgaacccc tccgcggaga ggagcgaggc 150  
 ggcgccaggg tggcccccg ggcgcgcttg gtctcggaga agcggggacg 200  
 aggccggagg atgagcgact gagggcgacg cgggcactga cgcgagttgg 250  
 ggccgcgact accggcagct gacagcgca tgagcgactc cccagagacg 300  
 ccctagcccc gtgtgcgcgc caggcggagc ggcaggtgg ggctgggctg 350



agtacacaaa agtacactat tatatatcaa atgtatttct ataatccctc 1850  
cattagagag cttatataag tgttttctat agatgcagat taaaaatgct 1900  
gtgttggtcaa ccgtcaaaaa aaaaaaaaaa aaaaaaaaaa aa 1942

<210> 11  
<211> 325  
<212> PRT  
<213> Homo sapiens

<400> 11  
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20 25 30  
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35 40 45  
Glu Lys Arg Glu His Ala Thr Arg Asp Gly Pro Gly Arg Val Asn  
50 55 60  
Glu Leu Gly Arg Pro Ala Arg Asp Glu Gly Gly Ser Gly Arg Asp  
65 70 75  
Trp Lys Ser Lys Ser Gly Arg Gly Leu Ala Gly Arg Glu Pro Trp  
80 85 90  
Ser Lys Leu Lys Gln Ala Trp Val Ser Gln Gly Gly Gly Ala Lys  
95 100 105  
Ala Gly Asp Leu Gln Val Arg Pro Arg Gly Asp Thr Pro Gln Ala  
110 115 120  
Glu Ala Leu Ala Ala Ala Ala Gln Asp Ala Ile Gly Pro Glu Leu  
125 130 135  
Ala Pro Thr Pro Glu Pro Pro Glu Glu Tyr Val Tyr Pro Asp Tyr  
140 145 150  
Arg Gly Lys Gly Cys Val Asp Glu Ser Gly Phe Val Tyr Ala Ile  
155 160 165  
Gly Glu Lys Phe Ala Pro Gly Pro Ser Ala Cys Pro Cys Leu Cys  
170 175 180  
Thr Glu Glu Gly Pro Leu Cys Ala Gln Pro Glu Cys Pro Arg Leu  
185 190 195  
His Pro Arg Cys Ile His Val Asp Thr Ser Gln Cys Cys Pro Gln  
200 205 210  
Cys Lys Glu Arg Lys Asn Tyr Cys Glu Phe Arg Gly Lys Thr Tyr  
215 220 225  
Gln Thr Leu Glu Glu Phe Val Val Ser Pro Cys Glu Arg Cys Arg

230	235	240
Cys Glu Ala Asn Gly Glu Val Leu Cys Thr Val Ser Ala Cys Pro		
245	250	255
Gln Thr Glu Cys Val Asp Pro Val Tyr Glu Pro Asp Gln Cys Cys		
260	265	270
Pro Ile Cys Lys Asn Gly Pro Asn Cys Phe Ala Glu Thr Ala Val		
275	280	285
Ile Pro Ala Gly Arg Glu Val Lys Thr Asp Glu Cys Thr Ile Cys		
290	295	300
His Cys Thr Tyr Glu Glu Gly Thr Trp Arg Ile Glu Arg Gln Ala		
305	310	315
Met Cys Thr Arg His Glu Cys Arg Gln Met		
320	325	

<210> 12  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 12  
 gaggtgtcgc tgtgaagcca acgg 24

<210> 13  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 13  
 cgctcgattc tccatgtgcc ttcc 24

<210> 14  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 14  
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<210> 15  
 <211> 1587  
 <212> DNA  
 <213> Homo sapiens

<400> 15

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gttcagcatg tgtggaaggt gtccgacctt ccccggaat ggaccctaa 150  
gaacaccagc tgcgacagcg gcttgggggt ccaggacacg ttgatgctca 200  
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aatggccttg gacaccagat tcttcccat tctgtccatg aatcatcttc 1450

cccacacaca atcattcata tctactcacc taacagcaac actggggaga 1500  
gcctggagca tccggacttg ccctatggga gaggggacgc tggaggagtg 1550  
gctgcatgta tctgataata cagaccctgt cctttca 1587

<210> 16  
<211> 437  
<212> PRT  
<213> Homo sapiens

<400> 16  
Met Ser Ala Val Leu Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro  
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20 25 30  
His Val Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys  
35 40 45  
Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met  
50 55 60  
Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly  
65 70 75  
Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg  
80 85 90  
Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg  
95 100 105  
Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp  
110 115 120  
Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val  
125 130 135  
Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile  
140 145 150  
Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu  
155 160 165  
Arg Gly Gly Gly Ile Phe Ser Asn Leu Arg Val Gln Gly Cys Met  
170 175 180  
Pro Gln Pro Gly Cys Asn Leu Leu Asn Gly Thr Gln Glu Ile Gly  
185 190 195  
Pro Val Gly Met Thr Glu Asn Cys Asn Arg Lys Asp Phe Leu Thr  
200 205 210  
Cys His Arg Gly Thr Thr Ile Met Thr His Gly Asn Leu Ala Gln  
215 220 225  
Glu Pro Thr Asp Trp Thr Thr Ser Asn Thr Glu Met Cys Glu Val



	230		235		240
Gly Gln Val Cys	Gln Glu Thr Leu Leu	Leu Ile Asp Val Gly Leu			
	245		250		255
Thr Ser Thr Leu	Val Gly Thr Lys Gly	Cys Ser Thr Val Gly Ala			
	260		265		270
Gln Asn Ser Gln	Lys Thr Thr Ile His	Ser Ala Pro Pro Gly Val			
	275		280		285
Leu Val Ala Ser	Tyr Thr His Phe Cys	Ser Ser Asp Leu Cys Asn			
	290		295		300
Ser Ala Ser Ser	Ser Ser Val Leu Leu	Asn Ser Leu Pro Pro Gln			
	305		310		315
Ala Ala Pro Val	Pro Gly Asp Arg Gln	Cys Pro Thr Cys Val Gln			
	320		325		330
Pro Leu Gly Thr	Cys Ser Ser Gly Ser	Pro Arg Met Thr Cys Pro			
	335		340		345
Arg Gly Ala Thr	His Cys Tyr Asp Gly	Tyr Ile His Leu Ser Gly			
	350		355		360
Gly Gly Leu Ser	Thr Lys Met Ser Ile	Gln Gly Cys Val Ala Gln			
	365		370		375
Pro Ser Ser Phe	Leu Leu Asn His Thr	Arg Gln Ile Gly Ile Phe			
	380		385		390
Ser Ala Arg Glu	Lys Arg Asp Val Gln	Pro Pro Ala Ser Gln His			
	395		400		405
Glu Gly Gly Gly	Ala Glu Gly Leu Glu	Ser Leu Thr Trp Gly Val			
	410		415		420
Gly Leu Ala Leu	Ala Pro Ala Leu Trp	Trp Gly Val Val Cys Pro			
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Ser Cys

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 <212> DNA  
 <213> Homo sapiens

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 ccaagactcg ctacgaggat gtcaaccccg tgctattgtc gggccccgag 200



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 <212> PRT  
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 Leu Ser Gly Pro Glu Ala Pro Trp Arg Asp Pro Glu Leu Leu Glu  
 65 70 75  
 Gly Thr Cys Thr Pro Val Gln Leu Val Ala Leu Ile Arg His Gly  
 80 85 90  
 Thr Arg Tyr Pro Thr Val Lys Gln Ile Arg Lys Leu Arg Gln Leu  
 95 100 105  
 His Gly Leu Leu Gln Ala Arg Gly Ser Arg Asp Gly Gly Ala Ser

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Leu Trp Tyr Ala Asp Trp Met Asp Gly	Gln Leu Val Glu Lys Gly	
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Arg Gln Asp Met Arg Gln Leu Ala Leu	Arg Leu Ala Ser Leu Phe	
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Pro Ala Leu Phe Ser Arg Glu Asn Tyr	Gly Arg Leu Arg Leu Ile	
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Thr Ser Ser Lys His Arg Cys Met Asp	Ser Ser Ala Ala Phe Leu	
185	190	195
Gln Gly Leu Trp Gln His Tyr His Pro	Gly Leu Pro Pro Pro Asp	
200	205	210
Val Ala Asp Met Glu Phe Gly Pro Pro	Thr Val Asn Asp Lys Leu	
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Met Arg Phe Phe Asp His Cys Glu Lys	Phe Leu Thr Glu Val Glu	
230	235	240
Lys Asn Ala Thr Ala Leu Tyr His Val	Glu Ala Phe Lys Thr Gly	
245	250	255
Pro Glu Met Gln Asn Ile Leu Lys Lys	Val Ala Ala Thr Leu Gln	
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Val Pro Val Asn Asp Leu Asn Ala Asp	Leu Ile Gln Val Ala Phe	
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Ser Ser Pro Val Ile Leu Gln Phe Gly	His Ala Glu Thr Leu Leu	
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Pro Leu Leu Ser Leu Met Gly Tyr Phe	Lys Asp Lys Glu Pro Leu	
380	385	390
Thr Ala Tyr Asn Tyr Lys Lys Gln Met	His Arg Lys Phe Arg Ser	
395	400	405

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 Thr Val Ser Phe Tyr Glu Asp Leu Lys Asn His Tyr Lys Asp Ile  
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<400> 20

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Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu
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Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr
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Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val
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				260					265					270
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro
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295

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&lt;210&gt; 21

&lt;211&gt; 3437

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

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 Ala Leu Ala Phe Arg Gln Asp Leu Glu Val Val Ser Ser Thr Val  
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 Arg Ser Pro His Leu Glu Glu Leu Leu Thr Ala Phe Phe Ser Ala

	395	400	405
Thr Ala Asp Ala	Ala Ser Pro Phe Pro	Ala Cys Lys Pro Val	Val
	410	415	420
Val Val Ser Ser	Leu Leu Leu Gln Glu	Glu Glu Pro Leu Ala	Gly
	425	430	435
Gly Lys Pro Gly	Ala Asp Gly Gly Ser	Leu Glu Ala Val Arg	Leu
	440	445	450
Gly Pro Ser Ser	Gly Leu Leu Val Asp	Trp Leu Glu Met Leu	Asp
	455	460	465
Pro Glu Val Val	Ser Ser Cys Pro Asp	Leu Gln Leu Arg Leu	Leu
	470	475	480
Phe Ser Arg Arg	Lys Gly Lys Gly Gln	Ala Gln Val Pro Ser	Phe
	485	490	495
Arg Pro Tyr Leu	Leu Thr Leu Phe Thr	His Gln Ser Ser Trp	Pro
	500	505	510
Thr Leu His Gln	Cys Ile Arg Val Leu	Leu Gly Lys Ser Arg	Glu
	515	520	525
Gln Arg Phe Asp	Pro Ser Ala Ser Leu	Asp Phe Leu Trp Ala	Cys
	530	535	540
Ile His Val Pro	Arg Ile Trp Gln Gly	Arg Asp Gln Arg Thr	Pro
	545	550	555
Gln Lys Arg Arg	Glu Glu Leu Val Leu	Arg Val Gln Gly Pro	Glu
	560	565	570
Leu Ile Ser Leu	Val Glu Leu Ile Leu	Ala Glu Ala Glu Thr	Arg
	575	580	585
Ser Gln Asp Gly	Asp Thr Ala Ala Cys	Ser Leu Ile Gln Ala	Arg
	590	595	600
Leu Pro Leu Leu	Leu Ser Cys Cys Cys	Gly Asp Asp Glu Ser	Val
	605	610	615
Arg Lys Val Thr	Glu His Leu Ser Gly	Cys Ile Gln Gln Trp	Gly
	620	625	630
Asp Ser Val Leu	Gly Arg Arg Cys Arg	Asp Leu Leu Leu Gln	Leu
	635	640	645
Tyr Leu Gln Arg	Pro Glu Leu Arg Val	Pro Val Pro Glu Val	Leu
	650	655	660
Leu His Ser Glu	Gly Ala Ala Ser Ser	Ser Val Cys Lys Leu	Asp
	665	670	675
Gly Leu Ile His	Arg Phe Ile Thr Leu	Leu Ala Asp Thr Ser	Asp
	680	685	690

Ser Arg Ala Leu	Glu Asn Arg Gly Ala	Asp Ala Ser Met Ala Cys
695	700	705
Arg Lys Leu <sup>s</sup> Ala	Val Ala His Pro Leu	Leu Leu Leu Arg His Leu
710	715	720
Pro Met Ile Ala	Ala Leu Leu His Gly	Arg Thr His Leu Asn Phe
725	730	735
Gln Glu Phe Arg	Gln Gln Asn His Leu	Ser Cys Phe Leu His Val
740	745	750
Leu Gly Leu Leu	Glu Leu Leu Gln Pro	His Val Phe Arg Ser Glu
755	760	765
His Gln Gly Ala	Leu Trp Asp Cys Leu	Leu Ser Phe Ile Arg Leu
770	775	780
Leu Leu Asn Tyr	Arg Lys Ser Ser Arg	His Leu Ala Ala Phe Ile
785	790	795
Asn Lys Phe Val	Gln Phe Ile His Lys	Tyr Ile Thr Tyr Asn Ala
800	805	810
Pro Ala Ala Ile	Ser Phe Leu Gln Lys	His Ala Asp Pro Leu His
815	820	825
Asp Leu Ser Phe	Asp Asn Ser Asp Leu	Val Met Leu Lys Ser Leu
830	835	840
Leu Ala Gly Leu	Ser Leu Pro Ser Arg	Asp Asp Arg Thr Asp Arg
845	850	855
Gly Leu Asp Glu	Glu Gly Glu Glu Glu	Ser Ser Ala Gly Ser Leu
860	865	870
Pro Leu Val Ser	Val Ser Leu Phe Thr	Pro Leu Thr Ala Ala Glu
875	880	885
Met Ala Pro Tyr	Met Lys Arg Leu Ser	Arg Gly Gln Thr Val Glu
890	895	900
Asp Leu Leu Glu	Val Leu Ser Asp Ile	Asp Glu Met Ser Arg Arg
905	910	915
Arg Pro Glu Ile	Leu Ser Phe Phe Ser	Thr Asn Leu Gln Arg Leu
920	925	930
Met Ser Ser Ala	Glu Glu Cys Cys Arg	Asn Leu Ala Phe Ser Leu
935	940	945
Ala Leu Arg Ser	Met Gln Asn Ser Pro	Ser Ile Ala Ala Ala Phe
950	955	960
Leu Pro Thr Phe	Met Tyr Cys Leu Gly	Ser Gln Asp Phe Glu Val
965	970	975
Val Gln Thr Ala	Leu Arg Asn Leu Pro	Glu Tyr Ala Leu Leu Cys

980	985	990
Gln Glu His Ala Ala Val Leu Leu His Arg Ala Phe Leu Val Gly		
995	1000	1005
Met Tyr Gly Gln Met Asp Pro Ser Ala Gln Ile Ser Glu Ala Leu		
1010	1015	1020
Arg Ile Leu His Met Glu Ala Val Met		
1025		

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 <211> 2186  
 <212> DNA  
 <213> Homo sapiens

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 cgccttctctc tcgctgtcct ggtacgcggc actcagcggc cagaaaggcg 150  
 acgttggtgga cgtttaccag cgggagttcc tggcgctgcg cgatcggttg 200  
 cacgcagctg agcaggagag cctcaagcgc tccaaggagc tcaacctggt 250  
 gctggacgag atcaagaggg ccgtgtcaga aaggcaggcg ctgcgagacg 300  
 gagacggcaa tcgcacctgg ggccgcctaa cagaggaccc ccgattgaag 350  
 ccgtggaacg gctcacaccg gcacgtgctg cacctgccca ccgtcttcca 400  
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 gcgtggggcca gggccgcacc ggagtgtcgg tggatgatggg catccccgagc 500  
 gtgcggcgcg aggtgcactc gtacctgact gacactctgc actcgctcat 550  
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 gccttggtcc ccacggagat ccattctggg ctctggagg tcattctacc 700  
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 ttctcatga tgtacgcgca gtccaaaggc atctactacg tgcagctgga 850  
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 cactgcagca gccttcagag gactggatga tcctggagtt ctcccagctg 950  
 ggcttcattg gtaagatgtt caagtcgctg gacctgagcc tgattgtaga 1000  
 gttcattctc atgttctacc gggacaagcc catcgactgg ctctggacc 1050

atattctgtg ggtgaaagtc tgcaaccccg agaaggatgc gaagcactgt 1100  
 gaccggcaga aagccaacct gcggtatccgc ttcaaaccgt ccctcttcca 1150  
 gcacgtgggc actcactcct cgctggctgg caagatccag aaactgaagg 1200  
 acaaagactt tggaaagcag gcgctgcgga aggagcatgt gaacccgcca 1250  
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 ttccgcagtg ggaacatcga gcacccggag gacaagctct tcaacacgtc 1450  
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 ggaggcccta ggagctggtg ctgccccgcg ccgcccggcc gcggaggagg 1900  
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 attcttggat acatttgatt ttttcacgta agtccacata tacttctata 2100  
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 <212> PRT  
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 Leu Cys Ala Phe Leu Ser Leu Ser Trp Tyr Ala Ala Leu Ser Gly  
 20 25 30



Gln Lys Gly Asp Val Val Asp Val Tyr Gln Arg Glu Phe Leu Ala  
 35 40 45  
 Leu Arg Asp Arg Leu His Ala Ala Glu Gln Glu Ser Leu Lys Arg  
 50 55 60  
 Ser Lys Glu Leu Asn Leu Val Leu Asp Glu Ile Lys Arg Ala Val  
 65 70 75  
 Ser Glu Arg Gln Ala Leu Arg Asp Gly Asp Gly Asn Arg Thr Trp  
 80 85 90  
 Gly Arg Leu Thr Glu Asp Pro Arg Leu Lys Pro Trp Asn Gly Ser  
 95 100 105  
 His Arg His Val Leu His Leu Pro Thr Val Phe His His Leu Pro  
 110 115 120  
 His Leu Leu Ala Lys Glu Ser Ser Leu Gln Pro Ala Val Arg Val  
 125 130 135  
 Gly Gln Gly Arg Thr Gly Val Ser Val Val Met Gly Ile Pro Ser  
 140 145 150  
 Val Arg Arg Glu Val His Ser Tyr Leu Thr Asp Thr Leu His Ser  
 155 160 165  
 Leu Ile Ser Glu Leu Ser Pro Gln Glu Lys Glu Asp Ser Val Ile  
 170 175 180  
 Val Val Leu Ile Ala Glu Thr Asp Ser Gln Tyr Thr Ser Ala Val  
 185 190 195  
 Thr Glu Asn Ile Lys Ala Leu Phe Pro Thr Glu Ile His Ser Gly  
 200 205 210  
 Leu Leu Glu Val Ile Ser Pro Ser Pro His Phe Tyr Pro Asp Phe  
 215 220 225  
 Ser Arg Leu Arg Glu Ser Phe Gly Asp Pro Lys Glu Arg Val Arg  
 230 235 240  
 Trp Arg Thr Lys Gln Asn Leu Asp Tyr Cys Phe Leu Met Met Tyr  
 245 250 255  
 Ala Gln Ser Lys Gly Ile Tyr Tyr Val Gln Leu Glu Asp Asp Ile  
 260 265 270  
 Val Ala Lys Pro Asn Tyr Leu Ser Thr Met Lys Asn Phe Ala Leu  
 275 280 285  
 Gln Gln Pro Ser Glu Asp Trp Met Ile Leu Glu Phe Ser Gln Leu  
 290 295 300  
 Gly Phe Ile Gly Lys Met Phe Lys Ser Leu Asp Leu Ser Leu Ile  
 305 310 315  
 Val Glu Phe Ile Leu Met Phe Tyr Arg Asp Lys Pro Ile Asp Trp

320	325	330
Leu Leu Asp His Ile Leu Trp Val Lys	Val Cys Asn Pro Glu Lys	
335	340	345
Asp Ala Lys His Cys Asp Arg Gln Lys	Ala Asn Leu Arg Ile Arg	
350	355	360
Phe Lys Pro Ser Leu Phe Gln His Val Gly Thr His Ser Ser Leu		
365	370	375
Ala Gly Lys Ile Gln Lys Leu Lys Asp Lys Asp Phe Gly Lys Gln		
380	385	390
Ala Leu Arg Lys Glu His Val Asn Pro Pro Ala Glu Val Ser Thr		
395	400	405
Ser Leu Lys Thr Tyr Gln His Phe Thr Leu Glu Lys Ala Tyr Leu		
410	415	420
Arg Glu Asp Phe Phe Trp Ala Phe Thr Pro Ala Ala Gly Asp Phe		
425	430	435
Ile Arg Phe Arg Phe Phe Gln Pro Leu Arg Leu Glu Arg Phe Phe		
440	445	450
Phe Arg Ser Gly Asn Ile Glu His Pro Glu Asp Lys Leu Phe Asn		
455	460	465
Thr Ser Val Glu Val Leu Pro Phe Asp Asn Pro Gln Ser Asp Lys		
470	475	480
Glu Ala Leu Gln Glu Gly Arg Thr Ala Thr Leu Arg Tyr Pro Arg		
485	490	495
Ser Pro Asp Gly Tyr Leu Gln Ile Gly Ser Phe Tyr Lys Gly Val		
500	505	510
Ala Glu Gly Glu Val Asp Pro Ala Phe Gly Pro Leu Glu Ala Leu		
515	520	525
Arg Leu Ser Ile Gln Thr Asp Ser Pro Val Trp Val Ile Leu Ser		
530	535	540
Glu Ile Phe Leu Lys Lys Ala Asp		
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<400> 31

ctgtggtacc caattgccgc cttgt 25

<210> 32

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 32

attgtcctga gattcgagca aga 23

<210> 33

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 33

gtccagcaag ccctcatt 18

<210> 34

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 34

cttctgggcc acagccctgc 20

<210> 35

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 35

cagttcaggt cgtttcattc a 21

<210> 36

<211> 19

<212> DNA

<213> Artificial Sequence

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attgtcctga gattcgagca aga 23  
gtccagcaag ccctcatt 18  
cttctgggcc acagccctgc 20  
cagttcaggt cgtttcattc a 21

